

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 12, 2003, 14:50:32 ; Search time 27 Seconds

(without alignments)  
1215.103 Million cell updates/sec

Title: US-09-804-472-2

Perfect score: 4177

Sequence: 1 MDASSDPYLPYDGGGNIPL.....DILRHMAQTANODPASIMFN 791\*

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3997	95.7	760	1	CLC3_CAVPO
2	3996	95.7	760	1	CLC3_MOUSE
3	3994	95.6	760	1	CLC3_RAT
4	3991	95.5	762	1	CLC3_HUMAN
5	3281	78.5	760	1	CLC4_HUMAN
6	3240	77.6	747	1	CLC4_RAT
7	3217	77.0	747	1	CLC4_MOUSE
8	3139.5	75.2	746	1	CLC5_HUMAN
9	3138.5	75.1	746	1	CLC5_RAT
10	3137.5	75.1	746	1	CLC5_MOUSE
11	996.5	23.9	779	1	GEET_YEAST
12	751	18.0	803	1	CLC7_MOUSE
13	751	18.0	803	1	CLC7_RAT
14	748.5	17.9	805	1	CLC7_HUMAN
15	725.5	17.4	869	1	CLC6_HUMAN
16	711	17.0	870	1	CLC6_MOUSE
17	658.5	15.8	902	1	CLC2_CAVPO
18	655.5	15.7	902	1	CLC2_HUMAN
19	652	15.6	907	1	CLC2_RAT
20	646	15.5	898	1	CLC2_RABIT
21	637.5	15.3	908	1	CLC2_MOUSE
22	602.5	14.4	994	1	CLC1_RAT
23	594.5	14.2	994	1	CLC1_MOUSE
24	591	14.1	809	1	CLC1_TORCA
25	590.5	14.1	805	1	CLC1_TORNA
26	579.5	13.9	888	1	CLC1_HUMAN
27	536	12.8	687	1	CLC1_RABIT
28	530.5	12.7	687	1	CLC1_HUMAN
29	530	12.7	687	1	CLC1_HUMAN
30	528	12.6	687	1	CLC1_RAT
31	516	12.4	678	1	CLC1_RABIT
32	504.5	12.1	687	1	CLC1_RAT
33	342.5	8.2	468	1	ERIC_VIBCH

## ALIGNMENTS

RESULT 1	CLC3_CAVPO	STANDARD:	PRT:	760 AA.
AC	Q9R279;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Chloride channel protein 3 (CLC-3).			
GN	CLC3.			
OS	Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.			
OX	NCBI_TaxID=10141;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Small intestine;			
RA	Varela D., Cid L.P., Sepulveda F.V.;			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
CC	- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE			
CC	SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;			
CC	MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND			
CC	TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL			
CC	CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY			
CC	PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-			
CC	TERM MEMORY (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.			
CC	- SIMILARITY: CONTAINS 2 CBS DOMAINS.			
CC	-----			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL: AF133214; AAD33599.1; -			
DR	InterPro: IPR000644; CBS.domain			
DR	InterPro: IPR001807; Cl_channel_volt.			
DR	Pfam: PF00571; CBS; 2.			
DR	Pfam: PF00654; Voltage_CLC; 1.			
DR	PRINTS: PR00762; CLCHANNEL.			
DR	SMART: SM00116; CBS; 2.			
KW	Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;			
KW	CBS domain; Repeat.			
FT	TRANSMEM 68			POTENTIAL.
FT	TRANSMEM 154			POTENTIAL.
FT	TRANSMEM 175			POTENTIAL.
FT	TRANSMEM 195			POTENTIAL.
FT	TRANSMEM 202			POTENTIAL.
FT	TRANSMEM 222			POTENTIAL.
FT	TRANSMEM 259			POTENTIAL.
FT	TRANSMEM 279			POTENTIAL.
FT	TRANSMEM 285			POTENTIAL.
FT	TRANSMEM 305			POTENTIAL.
FT	TRANSMEM 330			POTENTIAL.
FT	TRANSMEM 350			POTENTIAL.
FT	TRANSMEM 365			POTENTIAL.
FT	TRANSMEM 442			POTENTIAL.
FT	TRANSMEM 462			POTENTIAL.
FT	TRANSMEM 467			POTENTIAL.
FT	TRANSMEM 487			POTENTIAL.

34	304.5	7.3	473	1	ERIC_SALTI	O829b3 salmonella
35	304.5	7.3	473	1	ERIC_SALTY	O829b8 salmonella
36	294.5	7.1	478	1	ERIC_YERPE	O82bno yersinia pe
37	284.5	6.8	473	1	ERIC_ECOLI	P37019 escherichia
38	283.5	6.8	473	1	ERIC_ECO57	P58244 escherichia
39	260.5	6.2	461	1	ERIC_RALSO	O8xt44 ralsconia s
40	235	5.6	430	1	ERIC_YERPE	O82eb3 yersinia pe
41	230	5.5	429	1	ERIC_YERPS	O9agq5 yersinia ps
42	227.5	5.4	395	1	Y305_MERJA	O57753 methanococ
43	208	5.0	438	1	ERIC_ECO57	O8x794 escherichia
44	208	5.0	438	1	ERIC_ECOLI	P76175 escherichia
45	205	4.9	437	1	ERIC_SALTI	O826y0 salmonella

FT TRANSMEM 508 528 POTENTIAL.  
 FT TRANSMEM 536 556 POTENTIAL.  
 FT DOMAIN 599 659 CBS 1.  
 FT DOMAIN 696 747 CBS 2.  
 SQ SEQUENCE 760 AA: 84485 MM: BC2E2A5BE60B3D CRC64:

Query Match 95.7%; Score 3997; DB 1; Length 760;  
 Best Local Similarity 99.7%; Pred. No. 2.5e-278;  
 Matches 758; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 32 MTNGSGINSSHHLLDLDDEPIPGVGYDDFTIDWREKCKDRHRHRINSKKESAMEM 91  
 DB 1 MTNGSGINSSHHLLDLDDEPIPGVGYDDFTIDWREKCKDRHRHRINSKKESAMEM 60  
 QY 92 TKSLYDAMSGMLVYTLTGLASGALAGLIDADMMTDLKEGICLSALMYNEQCCWGSNE 151  
 DB 61 TKSLYDAMSGMLVYTLTGLASGALAGLIDADMMTDLKEGICLSALMYNEQCCWGSNE 120  
 QY 152 TTEPERKCPQWKTWABLLIGQAEQSGSYIMNYMIFWALSFAFLAVSLVKVPAPYACG 211  
 DB 121 TTEPERKCPQWKTWABLLIGQAEQSGSYIMNYMIFWALSFAFLAVSLVKVPAPYACG 180  
 QY 212 SGPEITILISGFIIRGLGKWTIMKITTLVLAASGLSGKEGPLYHVACCCGNFSY 271  
 DB 181 SGPEITILISGFIIRGLGKWTIMKITTLVLAASGLSGKEGPLYHVACCCGNFSY 240  
 QY 272 LEPYSTNEAKKREVLASASAGVAFGAPIGGVLSLEEVSYFPLKTLMSFFALV 331  
 DB 241 LEPYSTNEAKKREVLASASAGVAFGAPIGGVLSLEEVSYFPLKTLMSFFALV 300  
 QY 332 AAFVLRISINPFGNSRLVLFVEYHTPWYLFELPFILLVGFGIGWGAFFITANIAMCRR 391  
 DB 301 AAFVLRISINPFGNSRLVLFVEYHTPWYLFELPFILLVGFGIGWGAFFITANIAMCRR 360  
 QY 392 KSTFEGYPLEVETIYVAITVAFNPDPYRLNLTSELKELFTGCGPLESSLCDYRDM 451  
 DB 361 KSTFEGYPLEVETIYVAITVAFNPDPYRLNLTSELKELFTGCGPLESSLCDYRDM 420  
 QY 452 NASKIVDDIDPRPAGISVYSAIMOLCLALFKIMTVEFGIKVPSGLFIPSAIGAIA 511  
 DB 421 NASKIVDDIDPRPAGISVYSAIMOLCLALFKIMTVEFGIKVPSGLFIPSAIGAIA 480  
 QY 512 RIVGIANEOLAYYHHMFIFIREKCEVACDCTPCLYAMVGAACLGVTTRMTVSLVYIF 571  
 DB 481 RIVGIANEOLAYYHHMFIFIREKCEVACDCTPCLYAMVGAACLGVTTRMTVSLVYIF 540  
 QY 572 ELTGLGLYIYPLMAAVMTSKVGDPAFREGIYEAHIRLNGPPLDAKBEFTHTLADVM 631  
 DB 541 ELTGLGLYIYPLMAAVMTSKVGDPAFREGIYEAHIRLNGPPLDAKBEFTHTLADVM 600  
 QY 632 RPRRNDPPLAVLTQDNNVTVDIEMKINETSNGFPVIMSKESQRLVGFALRDLJTIAES 691  
 DB 601 RPRRNDPPLAVLTQDNNVTVDIEMKINETSNGFPVIMSKESQRLVGFALRDLJTIAES 660  
 QY 692 ARKQEBIVGSSRKCFAQHPSLPAPESPRLKLSIIDMSFTYTDTPMELTVDIRKL 751  
 DB 661 ARKQEBIVGSSRKCFAQHPSLPAPESPRLKLSIIDMSFTYTDTPMELTVDIRKL 720  
 QY 752 GLRQCLVTHNGRLIGITTKKDIERHMAOTANODPASIMFN 791  
 DB 721 GLRQCLVTHNGRLIGITTKKDIERHMAOTANODPASIMFN 760

RESULT 2  
 CLC3 MOUSE STANDARD; PRT; 760 AA.  
 ID CLC3 MOUSE  
 AC P51791;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Chloride channel protein 3 (CLC-3).  
 GN CLC3 OR CLC3.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxId=10090;  
 RX MEDLINE=95394449; PubMed=7665160;  
 RA Borsani G., Rugaili E.I., Tagliabata M., Wong C., Ballabio A.;  
 RT "Characterization of a human and murine gene (CLC3) sharing  
 RT similarities to voltage-gated chloride channels and to a yeast  
 RT integral membrane protein.";  
 RL Genomics 27:131-141(1995).  
 CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE  
 CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;  
 CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND  
 CC TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL  
 CC CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY  
 CC PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-  
 CC TERM MEMORY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE KIDNEY WHILE A  
 CC LOW LEVEL EXPRESSION IS SEEN IN THE BRAIN. WITHIN THE BRAIN, IT IS  
 CC PROMINENT IN THE HIPPOCAMPUS, CEREBRAL CORTEX AND OLFACTORY BULB.  
 CC -1- DEVELOPMENTAL STAGE: AT 10.5 DAYS OF DEVELOPMENT IT IS EXPRESSED  
 CC THROUGHOUT THE EMBRYO. LATER IN DEVELOPMENT (12.5 TO 14.5 DAYS OF  
 CC GESTATION), EXPRESSION IS PROGRESSIVELY UPREGULATED IN NEURONS OF  
 CC THE BRAIN AND THE SPINAL CORD, IN ALL CRANIAL SENSORY GANGLIA AND  
 CC IN THE SYMPATHETIC DORSAL ROOT GANGLIA.  
 CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL: X78874; CA55476.1; -  
 DR MGD: MG1:103555; Clcn3.  
 DR InterPro: IPR000644; CBS\_domain.  
 DR InterPro: IPR001807; Cl-channel\_volt.  
 DR Pfam: PF00571; CBS; 2.  
 DR Pfam: PF00654; voltage\_CLC; 1.  
 DR PRINTS: PR00762; CLCHANNEL.  
 DR SMART: SM00116; CBS; 2.  
 KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;  
 KW CBS domain; Repeat.  
 FT TRANSMEM 68 88 POTENTIAL.  
 FT TRANSMEM 154 174 POTENTIAL.  
 FT TRANSMEM 175 195 POTENTIAL.  
 FT TRANSMEM 202 222 POTENTIAL.  
 FT TRANSMEM 259 279 POTENTIAL.  
 FT TRANSMEM 285 305 POTENTIAL.  
 FT TRANSMEM 330 350 POTENTIAL.  
 FT TRANSMEM 365 385 POTENTIAL.  
 FT TRANSMEM 442 462 POTENTIAL.  
 FT TRANSMEM 467 487 POTENTIAL.  
 FT TRANSMEM 508 528 POTENTIAL.  
 FT TRANSMEM 536 556 POTENTIAL.  
 FT TRANSMEM 599 659 CBS 1.  
 FT DOMAIN 696 747 CBS 2.  
 FT VARIANT 653 653 D -> N.  
 SQ SEQUENCE 760 AA: 84475 MM: 0101C45A23509AFE CRC64:

Query Match 95.7%; Score 3996; DB 1; Length 760;  
 Best Local Similarity 99.7%; Pred. No. 3e-278;  
 Matches 758; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 32 MTNGSGINSSHHLLDLDDEPIPGVGYDDFTIDWREKCKDRHRHRINSKKESAMEM 91  
 DB 1 MTNGSGINSSHHLLDLDDEPIPGVGYDDFTIDWREKCKDRHRHRINSKKESAMEM 60

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QY 92 TKSLEYDAMSGMLVYVLTGLASGALAGLIDIAADWMTDEKIGICISALWYNHEOCCGWSNE 151
D 61 TKSLEYDAMSGMLVYVLTGLASGALAGLIDIAADWMTDEKIGICISALWYNHEOCCGWSNE 120
QY 152 TTFEERDKCPQWKTAWEELIIGQABSPGSYINMYIYFWALSFAFLAVSLVKVFPYACG 211
D 121 TTFEERDKCPQWKTAWEELIIGQABSPGSYINMYIYFWALSFAFLAVSLVKVFPYACG 180
QY 212 SGIPKIKTILSGFIIRGLGKWTLMIKITITLVAVASGLSGKEBPLVHVACCCGNIFS 271
D 181 SGIPKIKTILSGFIIRGLGKWTLMIKITITLVAVASGLSGKEBPLVHVACCCGNIFS 240
QY 272 LFPKSTNEAKKREVLASAASAGSVAFGAPIGVLFSLSESYFFPLKTLMRSEFALV 331
D 241 LFPKSTNEAKKREVLASAASAGSVAFGAPIGVLFSLSESYFFPLKTLMRSEFALV 300
QY 332 AAFVLRSTINPGRNSRLVLYFEYEHRTWYLFELFPILLGVFGGLMGAFPIRANIAMCRRR 391
D 301 AAFVLRSTINPGRNSRLVLYFEYEHRTWYLFELFPILLGVFGGLMGAFPIRANIAMCRRR 360
QY 392 KSTRKGKXPVEVITVAITVAIPNPTRLNSELKELFTDCGPLSSSLCDYRNDM 451
D 361 KSTRKGKXPVEVITVAITVAIPNPTRLNSELKELFTDCGPLSSSLCDYRNDM 420
QY 452 NASKIVDDIPDRPAGIGVYSAIMQCLALIFKIIWTFEFGIKVPSGLFIPSMAGIAG 511
D 421 NASKIVDDIPDRPAGIGVYSAIMQCLALIFKIIWTFEFGIKVPSGLFIPSMAGIAG 480
QY 512 RIVGIVAGQALAYHHDMWTFEKECEVAGDCITPGLIYANVGAACIGVTRMTVSLVIVF 571
D 481 RIVGIVAGQALAYHHDMWTFEKECEVAGDCITPGLIYANVGAACIGVTRMTVSLVIVF 540
QY 572 ELTGGLXIVPLMAAVMSKMWGDAFREGIYEAHIRLNGYPLDPAKEEFHTTLAAVYM 631
D 541 ELTGGLXIVPLMAAVMSKMWGDAFREGIYEAHIRLNGYPLDPAKEEFHTTLAAVYM 600
QY 632 RPRRNDPELAVLTODNMVDDIENMINETSYNGFPVIMSKESQRLVGFALRRDLTIAES 691
D 601 RPRRNDPELAVLTODNMVDDIENMINETSYNGFPVIMSKESQRLVGFALRRDLTIAES 660
QY 692 ARKKEGIVGSSRCFAQHTPSLPAESPRPLKLSIDMSPEFTVDTHTPMEIIVDIEFKL 751
D 661 ARKKEGIVGSSRCFAQHTPSLPAESPRPLKLSIDMSPEFTVDTHTPMEIIVDIEFKL 720
QY 752 GLRQCLVTHNGRLGLITTKKDLIRHMAOTANODPASIMFN 791
D 721 GLRQCLVTHNGRLGLITTKKDLIRHMAOTANODPASIMFN 760

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CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL
CC CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY
CC PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-
CC TERM MEMORY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, ESPECIALLY IN THE OLFACTORY
CC BULB, HIPPOCAMPUS, AND CEREBELLUM. A MODERATE EXPRESSION IS SEEN
CC IN THE LUNG, KIDNEY AND ADRENAL GLAND.
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC
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CC
CC -----
CC EMBL: D17521; BAA04471.1; -
CC InterPro: IPR000644; CBS_domain.
CC InterPro: IPR001807; Cl-channel_volt.
CC Pfam: PF00571; CBS; 2.
CC Pfam: PF00654; voltage_Clc; 1.
CC DR PRINTS: PR00762; CLCHANNEL.
CC SMART: SM00116; CBS; 2.
CC
CC Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
CC CBS domain; Repeat.
CC FT TRANSSEM 68 88 POTENTIAL.
CC FT TRANSSEM 154 174 POTENTIAL.
CC FT TRANSSEM 175 195 POTENTIAL.
CC FT TRANSSEM 202 222 POTENTIAL.
CC FT TRANSSEM 259 279 POTENTIAL.
CC FT TRANSSEM 285 305 POTENTIAL.
CC FT TRANSSEM 330 350 POTENTIAL.
CC FT TRANSSEM 365 385 POTENTIAL.
CC FT TRANSSEM 442 462 POTENTIAL.
CC FT TRANSSEM 467 487 POTENTIAL.
CC FT TRANSSEM 508 528 POTENTIAL.
CC FT TRANSSEM 536 556 POTENTIAL.
CC FT DOMAIN 599 659 CBS 1.
CC FT DOMAIN 696 747 CBS 2.
CC SO SEQUENCE 760 AA; 84447 MW; 8A826FCA2497269C CMC64;

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Query Match 95.6%; Score 3994; DB 1; Length 760;
Best Local Similarity 99.5%; Pred. No. 4.1e-278;
Matches 756; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 32 MTNGSTNSSTHLDLDEPIGVGTVDPTHTIDVREKCKDREHRRIRNSKKKESAMEM 91
D 1 MTNGSTNSSTHLDLDEPIGVGTVDPTHTIDVREKCKDREHRRIRNSKKKESAMEM 60
QY 92 TKSLEYDAMSGMLVYVLTGLASGALAGLIDIAADWMTDEKIGICISALWYNHEOCCGWSNE 151
D 61 TKSLEYDAMSGMLVYVLTGLASGALAGLIDIAADWMTDEKIGICISALWYNHEOCCGWSNE 120
QY 152 TTFEERDKCPQWKTAWEELIIGQABSPGSYINMYIYFWALSFAFLAVSLVKVFPYACG 211
D 121 TTFEERDKCPQWKTAWEELIIGQABSPGSYINMYIYFWALSFAFLAVSLVKVFPYACG 180
QY 212 SGIPKIKTILSGFIIRGLGKWTLMIKITITLVAVASGLSGKEBPLVHVACCCGNIFS 271
D 181 SGIPKIKTILSGFIIRGLGKWTLMIKITITLVAVASGLSGKEBPLVHVACCCGNIFS 240
QY 272 LFPKSTNEAKKREVLASAASAGSVAFGAPIGVLFSLSESYFFPLKTLMRSEFALV 331
D 241 LFPKSTNEAKKREVLASAASAGSVAFGAPIGVLFSLSESYFFPLKTLMRSEFALV 300
QY 332 AAFVLRSTINPGRNSRLVLYFEYEHRTWYLFELFPILLGVFGGLMGAFPIRANIAMCRRR 391
D 301 AAFVLRSTINPGRNSRLVLYFEYEHRTWYLFELFPILLGVFGGLMGAFPIRANIAMCRRR 360

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OY 452 NSKIVDDIPDRPAGIGVYSAIMWCLALIFKIMTVTFEGIKVPSGLFIPSAIGAIG 511
CC |||
CC 421 NSKIVDDIPDRPAGIGVYSAIMWCLALIFKIMTVTFEGIKVPSGLFIPSAIGAIG 480
Db |||
OY 512 RIVGIVAEQALAYHHHMFIFKEKCEVAGADCTITGLYAMGAACLCGVTRMYSLVYIVF 511
CC |||
CC 481 RIVGIVAEQALAYHHHMFIFKEKCEVAGADCTITGLYAMGAACLCGVTRMYSLVYIVF 540
Db |||
OY 572 ELTGGLYEVLPMAAAMTSGKWDAGREGIYEAHRLNGYPLDLAKE--EFHHTLAD 629
CC |||
CC 541 ELTGGLYEVLPMAAAMTSGKWDAGREGIYEAHRLNGYPLDLAKEEFHHTLAD 600
Db |||
OY 630 VMRRNDPPLAVLTODNMTVDIENNINETSNGFPVIMSKESQRLVGFALRDLTIAI 689
CC |||
CC 601 VMRRNDPPLAVLTODNMTVDIENNINETSNGFPVIMSKESQRLVGFALRDLTIAI 660
Db |||
OY 690 ESARKKQEGIVSSRYCFQOHPSPSPAESPRPLKRSIILDMSEFTVTDHTPMEIVDIFR 749
CC |||
CC 661 ESARKKQEGIVSSRYCFQOHPSPSPAESPRPLKRSIILDMSEFTVTDHTPMEIVDIFR 720
Db |||
OY 750 KIGLRQCLVTHNGRLGILITTKKDIILRHMAOTANODPASIMFN 791
CC |||
Db 721 KIGLRQCLVTHNGRLGILITTKKDIILRHMAOTANODPASIMFN 762

RESULT 5
CLC4_HUMAN
ID CLC4_HUMAN STANDARD: PRT: 760 AA.
AC P51793; Q9UBU1;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 4 (CLC-4).
GN CLC4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Retina.
RC TISSUE=Retina.
RA MEDLINE=94348498; PubMed=8069296;
RA van Slegtenhorst M.A., Bassi M.T., Borsani G., Wapenaar M.C.,
RA Ferrero G.B., de Conchillos L., Rugaril E.I., Grillo A., Franco B.,
RA Zoghbi H.Y., Ballabio A.;
RT "A gene from the Xp22.3 region shares homology with voltage-gated
RT chloride channels";
RL Hum. Mol. Genet. 3:547-552(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=20035030; PubMed=10564087;
RA Kawasaki M., Fukuma T., Yamauchi K., Sakamoto H., Marumo F.,
RA Sasaki S.;
RT "Identification of an acid-activated Cl- channel from human skeletal
RT muscles";
RL Am. J. Physiol. 277:C948-C954(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens epithelium;
RA Rae J.L.;
RT "A chloride channel (CLC-4) in human lens epithelium";
RT Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPTHELIAL TRANSPORT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN SKELETAL MUSCLE AND ALSO
CC DETECTABLE IN BRAIN AND HEART.
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X77197; CA54417.1; -
CC EMBL: AB019432; BA477327.1; -
CC EMBL: AF170492; AAD50981.1; -
CC Genew: HGNC:2022; CLCNA.
CC MIM: 302910; -
CC InterPro: IPR000644; CBS domain.
CC InterPro: IPR001807; Cl-channel_volt.
CC Pfam: PF00571; CBS; 2.
CC Pfam: PF00554; voltage_CLC; 1.
CC PRINTS: PR00762; CLCHANNEL.
CC SMART: SM00116; CBS; 2.
CC K1 Ion channel; Ion transport; Voltage-gated channel; Transmembrane;
CC K2 CBS domain; Repeat.
CC FT TRANSMEM 68 88 POTENTIAL.
CC FT TRANSMEM 148 168 POTENTIAL.
CC FT TRANSMEM 202 222 POTENTIAL.
CC FT TRANSMEM 259 279 POTENTIAL.
CC FT TRANSMEM 330 350 POTENTIAL.
CC FT TRANSMEM 365 385 POTENTIAL.
CC FT TRANSMEM 442 462 POTENTIAL.
CC FT TRANSMEM 467 487 POTENTIAL.
CC FT TRANSMEM 508 528 POTENTIAL.
CC FT TRANSMEM 535 555 POTENTIAL.
CC FT DOMAIN 599 659 CBS 1.
CC FT DOMAIN 697 747 CBS 2.
CC FT CONFLICT 178 178 A -> R (IN REF. 1).
CC FT CONFLICT 498 499 II -> YY (IN REF. 1).
CC FT CONFLICT 659 659 K -> N (IN REF. 1).
CC SQ SEQUENCE 760 AA: 84916 MW: 345A25D1FEF3F217 CRC64;

Query Match 78.5%; Score 3281; DB:1; Length 760;
Best Local Similarity 78.2%; Pred. No. 4,2e-227;
Matches 594; Conservative 83; Mismatches 83; Indels 0; Gaps 0;

OY 32 MTNGGSINSTHLLDLEDEIPGVGTDPHTIDWVREKCKDERRRRIRSKKESAWEM 91
Db 1 MVAAGAMSGSGNLMDPLDEFPVGVTEDEPHTIDMLREKSRDIDRRKRTSKKESIEWE 60
OY 92 TNSLYDAMSGWLVTLTGLASGALAGLIDIAADMWDLAEGICLSALWYNHEQCGWSNE 151
Db 61 IKSLLDAMSGWVVMLLIGLAGTLAGVIDLAVDMWMDLKEGVCLSAFWVSHQCCWTSNE 120
OY 152 TTFEERDKCPOMKTMALLIIGQAGEGSYIMNYIMVIFNALSAFLAVSLVKFAVACG 211
Db 121 TTFEERDKCPOMKTMALLIIGQAGEGSYIMNYIMVIFNALSAFLAVSLVKFAVACG 180
OY 212 SGPEIKTILSGFTIRGYLGKMTLKITITLVAVASGLSKEGCVLVHACCCGNFSY 271
Db 181 SGPEIKTILSGFTIRGYLGKMTLKITITLVAVASGLSKEGCVLVHACCCGNFSY 240
OY 272 LPPKYSTNEAKKREVLSAASAGVSAFGAPIGVLFSLEEVSYRPLKTLWRSFPAALV 331
Db 241 LPPKYSTNEAKKREVLSAASAGVSAFGAPIGVLFSLEEVSYRPLKTLWRSFPAALV 300
OY 332 AAFVLSINPFGSRVLVEVYHTPWYLFELPEPITLGVFGGLKMAFFRAIACRR 391
Db 301 AAFVLSINPFGSRVLVEVYHTPWYLFELPEPITLGVFGGLKMAFFRAIACRR 360
OY 392 KSTKFGKYVLEVIYAATAVAIPNPYRNLTSLEIKELFDDCPLESSLDCVDRNDM 451
Db 361 KSTRKGYVLEVIYAATAVAIPNPYRNLTSLEIKELFDDCPLESSLDCVDRNDM 420
OY 452 NSKIVDDIPDRPAGIGVYSAIMWCLALIFKIMTVTFEGIKVPSGLFIPSAIGAIG 511
Db 421 NSKIVDDIPDRPAGIGVYSAIMWCLALIFKIMTVTFEGIKVPSGLFIPSAIGAIG 480

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DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 4 (CLC4-4).
GN CLC4 OR CLCN4-2 OR CLC4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=95400329; PubMed=7670496;
RA Ruygari E.I., Adler D.A., Borsani G., Tsuchiya K., Franco B.,
RA Hauge X., Distchev C., Chapman V., Ballabio A.;
RT "Different chromosomal localization of the Clcn4 gene in Mus spretus
RL and C57BL/6J mice."
RL Nat. Genet. 10:466-471(1995).
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL; Z49916; CA90150.1; .
DR MGD; MG1:104571; CLCN4-2.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR001807; CL-channel_volt.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR SMART; SM00116; CBS; 2.
DR Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW CBS domain; Repeat.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 135 155 POTENTIAL.
FT TRANSMEM 189 209 POTENTIAL.
FT TRANSMEM 246 266 POTENTIAL.
FT TRANSMEM 317 337 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
FT TRANSMEM 429 449 POTENTIAL.
FT TRANSMEM 454 474 POTENTIAL.
FT TRANSMEM 495 515 POTENTIAL.
FT TRANSMEM 522 542 POTENTIAL.
FT TRANSMEM 586 646 POTENTIAL.
FT DOMAIN CBS 1.
FT DOMAIN 684 734 CBS 2.
FT SEQUENCE 747 AA; 83974 MW; B5486A4A1B0721144 CRC64;

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Query Match          77.0%: Score 3217: DB 1: Length 747:
Best Local Similarity 77.6%: Pred. No. 1,5e-22;
Matches 580: Conservative 83: Mismatches 84: Indels 0: Gaps 0:

QY 45 LLDLDEPIPGTVDDEFTIDMVRKCKDKDRHRHRSKKKESAWEMTKSLYDANGMLV 104
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MDLEFPDPDVGTEDEFTIDMLRKSKSDTDHRRITKSKSEIWEFTKSLDAAKSGWV 60

QY 105 VTNLGSLAGLAGLIDIDADMMTDLKEGICLSALYVNHOCQWGSNETTFEERDKCPOMK 164
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 MLILGLAGTLAGVIDLAVDMMTDLKEGVCLSAFYSHQCCMTSNETTFEERDKCPIMQ 120

QY 165 TWALLIQAGAGPGSYINMYIMYIFWALSFPAFLAVSLVKVFAFYAGSGSPEIKTILSGF 224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 KMSLLLSQSSGASAYILINYLIMYLIMALLFPFLAVSLYRVFAFYACGSGSIPKIKTILSGF 180

```

QY	225	IIRGLGWTLMTIKITITVLVAVASGLSGREGPLVHAACCGNIFSVLPFRYSINAEKKR	284
Db	181	IIRGLGWTLTLKITVLIVLVAVSSGLSGKRGPLVHAACCGNFSSLSFYSKINEEKR	240
QY	285	EVLASAAGVAAGVAFGAFIGGVLSLEEVSYYPFLKTLMSRFFAALAAEFLRSINFGN	344
Db	241	EVLASAAAAGVAVAFGARIGGVLSLEEVSYYPFLKTLMSRFFAALAAEFLRSINFGN	300
QY	345	SRVLVEYEHYTPWYLFELPPFLLGVFGGLMGAFETIRANIAMCRKKSTKFGKYPVLEV	404
Db	301	SRVLVEYEHYTPWYLMELPFILLGVFGGLMGTLFTIRANIAMCRKKRTILRGKYPVLEV	360
QY	405	IIVAAITAVIAFPNRYPRNLNSELKELFTDCGGLLESSLCDYRNDNMNAKIYDDIPDR	464
Db	361	IAVTAVTAVIAYPNDRYQSTSELSIELFNCGGLESSQCDYLDNDNMNRPVDDIPDR	420
QY	465	AGIGVYSAINVOLCLALIFKIMVFEFTGKIKVPSGLFTPSMAIGAIAGRIGVIAEQLAY	524
Db	421	AGVGYYTAMQDLALALYKRIYITFTFGMKIRPSGLFTIPSMANVGMAARMVGIYGEQLAYH	480
QY	525	HHDFIFKEWCDEVGADCTITPGLYAVMGAAACLGCVTRATVSLVIVELFTGLEYIVPLM	584
Db	481	HHDMTIFERNMCRPGADCYTPGLYAVMGAAACLGCVTRMTVSIIVIMELTGGLEYIVPLM	540
QY	585	AAVMYSKVVGAFAFGEGYIEAHILNGLNRPFLDAAEFEFTHTTLADVYMRPRNDPPLAVLT	644
Db	541	AAAVYSKVVAAVAFGEGYIEAHILNGLNRPFLDYVDETHTRLTADVYMRPREEDPSVLVT	600
QY	645	QDNMTVDDIENNINETSINGSPVYIMSKESQPLVGFALRRDITLIIESARKKOEIVGSSR	704
Db	601	QDSMTVEVELLIKETYDNGFPVLVYSRSESLIGFAQRRELLAIKNAAROREIVYNSI	660
QY	705	VCEAQTNPESLPAESRPLKLSILDMSPFTVTDHTPMEIYVDIIFRKLGRLQCVLTNGRL	764
Db	661	MYFTEEPPELPAANSBPLKTLRIENLSPFTVTDHTPMEIYVDIIFRKLGRLQCVLTNSGR	720
QY	765	LGITTKDILRHMAQTANODPASIMEN	791
Db	721	LGITTKDVLRRHMAOMANODESIMEIN	747

RESULT 8			
ID	CLIC5_HUMAN	STANDARD;	PRT; 746 AA.
AC	P51795.		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Chloride channel protein 5 (CLIC-5).		
GN	CLIC5 OR CLIC2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney.		
RX	MEDLINE=96121370; Pubmed=8575751.		
RA	Fisher S.E., van Bakel I., Lloyd S.E., Pearce S.H.S.,		
RA	Thakker R.V., Craig I.W., Lloyd S.E., Pearce S.H.S.,		
RT	"Cloning and characterization of CLIC5, the human kidney chloride		
RT	"channel gene implicated in Dent disease (an X-linked hereditary		
RT	nephrolithiasis).";		
RL	Genomics 29:598-606(1995).		
RM	[2]		
RP	SEQUENCE OF 487-746 FROM N.A.		
RC	TISSUE=Kidney.		
RX	MEDLINE=95179126; Pubmed=7874126;		
RA	Fisher S., Black G.C.M., Lloyd S.E., Hatchwell E., Wrong O.,		
RA	Thakker R.V., Craig I.W., Lloyd S.E., Hatchwell E., Wrong O.,		
RT	"Isolation and partial characterization of a chloride channel gene		
RT	which is expressed in kidney and is a candidate for Dent's disease		
RT	(an X-linked hereditary nephrolithiasis).";		

RL Hum. Mol. Genet. 3:2053-2059(1994).  
RN [3]  
RP TISSUE SPECIFICITY.  
RC TISSUE=Vascular smooth muscle, and Aortic endothelium;  
RX MEDLINE=99222497; PubMed=10198195;  
RA Lamb F.S., Clayton G.H., Liu B.-X., Smith R.L., Barna T.J.,  
RA Schutte B.C.;  
RT "Expression of CLCN voltage-gated chloride channel genes in human  
RT blood vessels".  
RL J. Mol. Cell. Cardiol. 31:657-666(1999).  
RN [4]  
RP VARIANTS NPML ARG-200; LEU-244; GLU-506 AND PRO-520.  
RX MEDLINE=96158876; PubMed=8559248;  
RA Lloyd S.E., Pearce S.H.S., Fisher S.E., Steinmeyer K., Schwappach B.,  
RA Schelman S.J., Harding B., Bolino A., Devoto P.,  
RA Rigden S.P.A., Wrong O., Jentsch T.J., Craig I.W., Thakker R.V.;  
RT "A common molecular basis for three inherited kidney stone diseases".  
RL Nature 379:445-449(1996).  
RN [5]  
RP VARIANTS NPML.  
RX MEDLINE=97402204; PubMed=9259268;  
RA Lloyd S.E., Guenther W., Pearce S.H.S., Thomson A., Bianchi M.L.,  
RA Bosio M., Craig I.W., Fisher S.E., Schelman S.J., Wrong O.,  
RA Jentsch T.J., Thakker R.V.;  
RT "Characterisation of renal chloride channel, CLCN5, mutations in  
RT hypercalcaemic nephrolithiasis (kidney stones) disorders".  
RL Hum. Mol. Genet. 6:1233-1239(1997).  
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE  
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;  
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND  
CC TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN RENAL  
CC TUBULAR FUNCTION.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: KIDNEY. MODERATELY EXPRESSED IN AORTIC  
CC VASCULAR SMOOTH MUSCLE AND ENDOTHELIAL CELLS, AND AT A SLIGHTLY  
CC HIGHER LEVEL IN THE CORONARY VASCULAR SMOOTH MUSCLE.  
CC -1- DISEASE: DEFECTS IN CLCN5 ARE THE CAUSE OF FOUR DISORDERS OF  
CC HEREDITARY HYPERCALCAEMIC NEPHROLITHIASIS (KIDNEY STONES), THAT  
CC HAVE BEEN REFERRED TO AS DENT'S DISEASE (DD), X-LINKED RECESSIVE  
CC NEPHROLITHIASIS (XNL), X-LINKED RECESSIVE HYPOPHOSPHATEMIC  
CC RICKETS (XLRH) AND IDIOPATHIC LOW MOLECULAR WEIGHT PROTEINURIA OF  
CC JAPANESE CHILDREN (JILP). ALL FOUR DISEASES REPRESENT RENAL  
CC TUBULAR DISORDERS THEY ARE CHARACTERIZED BY LOW MOLECULAR WEIGHT  
CC PROTEINURIA, HYPERCALCAEMIA, NEPHROCALCINOSIS, NEPHROLITHIASIS  
CC (KIDNEY STONES) AND RENAL FAILURE. DD IS A FORM OF FANCONI  
CC SYNDROME (ALSO KNOWN AS X-LINKED RECESSIVE NEPHROLITHIASIS TYPE 2  
CC (NPHL2)).  
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.  
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.  
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CC -----  
DR EMBL: X91906; CA63000.1; -;  
DR EMBL: X81836; CA57430.1; -;  
DR Genew: HGNC:2023; CLCN5.  
DR MIM: 300008; -;  
DR MIM: 300009; -;  
DR MIM: 310468; -;  
DR InterPro: IPR000644; CBS\_domain.  
DR InterPro: IPR001807; CL\_channel\_volt.  
DR Pfam: PF00571; CBS; 2.  
DR Pfam: PF00654; voltage\_CLC; 1.  
DR PRINTS: PR00762; CLCHANNEL.  
DR SMART: SM00116; CBS; 2.  
KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;  
KW CBS domain; Repeat; Disease mutation.  
FT TRANSMEM 55 75 POTENTIAL.

FT TRANSMEM 133 153 POTENTIAL.  
FT TRANSMEM 189 209 POTENTIAL.  
FT TRANSMEM 246 266 POTENTIAL.  
FT TRANSMEM 317 337 POTENTIAL.  
FT TRANSMEM 352 372 POTENTIAL.  
FT TRANSMEM 428 448 POTENTIAL.  
FT TRANSMEM 453 473 POTENTIAL.  
FT TRANSMEM 494 514 POTENTIAL.  
FT TRANSMEM 521 541 POTENTIAL.  
FT DOMAIN 585 645 CBS 1.  
FT DOMAIN 682 733 CBS 2.  
FT DOMAIN 730 800 CBS 3.  
FT VARIANT 57 57 /R-> RH (IN DD).  
FT VARIANT 200 200 /Rtid=VAR\_001615.  
FT VARIANT 200 200 G-> V (IN DD).  
FT VARIANT 244 244 L-> R (IN NPML2).  
FT VARIANT 280 280 /Rtid=VAR\_001617.  
FT VARIANT 506 506 S-> L (IN NPML3).  
FT VARIANT 512 512 R-> P (IN JILP).  
FT VARIANT 520 520 /Rtid=VAR\_001619.  
FT VARIANT 527 527 G-> E (IN NPML1).  
FT VARIANT 527 527 /Rtid=VAR\_001620.  
FT VARIANT 527 527 G-> R (IN DD). ABOLISHES THE CHLORIDE  
FT VARIANT 527 527 CURRENTS).  
FT VARIANT 527 527 /Rtid=VAR\_001621.  
FT VARIANT 527 527 S-> P (IN NPML2).  
FT VARIANT 527 527 /Rtid=VAR\_001622.  
FT VARIANT 527 527 E-> D (IN DD). ABOLISHES THE CHLORIDE  
FT VARIANT 527 527 CURRENTS AND TOTAL LOSS OF FUNCTION).  
FT VARIANT 527 527 /Rtid=VAR\_001623.  
SQ SEQUENCE 746 AA; 83146 MW; EF913C5BA40C85D8 CRC64;  
Query Match 75.2%; Score 3139.5; DB 1; Length 746;  
Best Local Similarity 76.7%; Pred. No. 5.4e-217;  
Matches 573; Conservative 85; Mismatches 88; Indels 1; Gaps 1;  
45 LDLDDEPIPGVTDDEFTIDMVEREKCRHRHRIRNSKKESAWEMTKSLDAMSGWL 104  
1 MDLFEPIPGVTDDEFTIDMVEREKSRDRHRIRITKSKESWALHVSADAFSGRL 60  
105 VTGLGASGALGLIDNADMTDLKESICLSALYNNHCCGWSNETFEEROKCPWK 164  
61 MLTGLGSLGSLAGLIDISAHMMTDLKESICGGEFNEHCSEHVTFEEROKCPWN 120  
165 TWAELTIGQAGPSGYIMNYIMYFMALSPFAVLAVTKVAPYACGSGIPEITLISGF 224  
121 SMSQLITSDGAFAYIVNYFMVLMALFAFLAVSLKVFAPYACGSGIPEITLISGF 180  
225 IIRGLGKMTLMIRITLVLAVASGLSLGKCGPLVHVACCGNIFSYLFPRYSTNEAKR 284  
181 IIRGLGKMTLVITITVLAVSSGLSLGKCGPLVHVACCGNILCHCFNNYRKNRAKR 240  
285 EVLSNAGSANGVAPGAPIGVLFSEVSYFFPKLTMRSEFALVAAYVLRISINPGN 344  
241 EVLSNAGSANGVAPGAPIGVLFSEVSYFFPKLTMRSEFALVAAYVLRISINPGN 300  
345 SRLVLFVEYHTPWLPFLPFLITLGVGGLMGAFITANTAMORRRKSTFGYPLVEV 404  
301 SRLVLFVEYHTPWLPFLPFLITLGVGGLMGAFITANTAMORRRKSTFGYPLVEV 360  
405 IIVAITAVIAFPNPTRLNTSELIKELFTDCGLPLESSSLCDYRNDNASKITVDIDPR 464  
361 LVTAITAITLAFPNBYTMTSELISLFCNGLDSSKLCDEYRNTSK-GEGLDRP 419  
465 AGIGVYSATWOLCLALFKIIMTVFTGKIKVPSGLFIPSMAGIAGIAGVIAEOLAY 524  
420 AGGVYSAMWOLALTLILKIVITFTGKIPSGLFIPTSMAGIAGIAGVIAEOLAY 479  
525 HHDFIRKEWCEVADCTTPTGLVAMVGAACLGVTNTVSLVYIVETLGGLEYIPLM 584  
480 HOEMTIVENSWSGADCTTPTGLVAMVGAACLGVTNTVSLVYIVETLGGLEYIPLM 539



QY	585	AAVMSKVVGDFAEGEGEYIEAHIRLNGPELDAKEEFTHTLAAVVRNRNDPLAYLT	644
Db	540	AAAMTSKVVADALGEGEYIDAHIRLNGPELDAKEEFAKHTLAMDVKEFRNRDPLLTLYLT	599
QY	645	QDNMTVDDIEENNINNTSYNGEPVINSKESQRLVGFALRDLTLTIAESARKKQEGIVGSSR	704
Db	600	QDSMTVEDEVETIISFTYTSYSGFPVVVSRESQRLVGFALRDLTLTIAENARKKQGVVSTI	659
QY	705	VCFADHTSPLAESRPPLKRSILDSMSPPTVTDHTPMEIVDIFRKLGRQCLVTHNGRL	764
Db	660	IYFTEHSPEPLPYETPTLKRNLILDSPEFTVDTLPMETIVDIFRKLGRQCLVTHNGRL	719
QY	765	LGITRKDLIRHMAOTANODPASIMEN	791
Db	720	LGITRKDLVKHIAQMANODPDSILFN	746
RESULT 9			
CLC5_RAT			
ID	CLC5_RAT	STANDARD:	PRT: 746 AA.
AC	P51796;	P70642;	
DT	01-OCT-1996	(Rel. 34, Created)	
DT	01-OCT-1996	(Rel. 34, Last sequence update)	
DT	15-JUN-2002	(Rel. 41, Last annotation update)	
DE	Chloride channel protein 5 (CLC-5).		
GN	CLC5.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RC	MEDLINE=96125100; PubMed=8537281;		
RA	Sakamoto H., Kawasaki M., Uchida S., Sasaki S., Marumo F.;		
RT	"Identification of a new outwardly rectifying Cl- channel that belongs to a subfamily of the ClC Cl- channels.";		
RL	J. Biol. Chem. 271:10210-10216(1996).		
CC	-1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME; MEMBERNE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND TRANSPIRHEIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN RENAL TUBULAR FUNCTION.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- TISSUE SPECIFICITY: KIDNEY-SPECIFIC.		
CC	-1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.		
CC	-1- SIMILARITY: CONTAINS 2 CBS DOMAINS.		
CC	-----		
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CC	-----		
DR	EMBL;	Z56377;	CAA91216.1; -;
DR	EMBL;	D50497;	BAA09091.1; -;
DR	InterPro;	IPR000644;	CBS_domain.
DR	InterPro;	IPR001807;	Cl-channel_volt.
DR	Pfam;	PF00571;	CBS; 2.
DR	Pfam;	PF00654;	voltage_CLC; 1.
DR	PRINTS;	PR00762;	CLCHANNEL.
DR	SMART;	SM00116;	CBS; 2.
FW	Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;		

KW	CBS domain; Repeat.	POTENTIAL.
FT	TRANSMEM 55 75	POTENTIAL.
FT	TRANSMEM 133 153	POTENTIAL.
FT	TRANSMEM 189 209	POTENTIAL.
FT	TRANSMEM 246 266	POTENTIAL.
FT	TRANSMEM 317 337	POTENTIAL.
FT	TRANSMEM 352 372	POTENTIAL.
FT	TRANSMEM 428 448	POTENTIAL.
FT	TRANSMEM 453 473	POTENTIAL.
FT	TRANSMEM 494 514	POTENTIAL.
FT	TRANSMEM 521 541	POTENTIAL.
FT	DOMAIN 585 614	CBS 1.
FT	DOMAIN 682 733	CBS 2.
FT	CONFLICT 315 315	H -> Y (IN REF. 2).
Q0	SEQUENCE 746 AA; 83067 MW; 5F7D45F397003CE CRC64;	

Query Match	75.1%	Score 3138.5	DB 1	Length 746
Best Local Similarity	76.6%	Pred. No. 6.3e-217		
Matches	572	Conservative	86	Mismatches 86; Indels 1; Gaps 1
QY 45	LDLDEIPGVGYDDFTIDWRECKCDREHRRIRNSKKKESAMEMTKSLYDAMSGMLV	104		
Db 1	MDPLEEPIGVGYDDFTIDWREKSDROHREITKSSKSTALLHSVDASFQWML	60		
QY 105	VTLGLASGALAGLIDLDADMNTDLKEGICLSALYVNHQCCWGSNETTFEERDKCPQK	164		
Db 61	MLLGLLGSGLAGLIDISAHMNTDLKEICGGGFENHEHCCMSEHVFEDRDKPEVN	120		
QY 165	TWAEELIQAGEGPSYINMYIYMAFLASFLAVSVKVFAPYAGSGSIPETKITLSGF	224		
Db 121	SMQSILISTDGAFAFYIYNYEMVIMALLFALVAYLVKAFAPYAGSGSIPETKITLSGF	180		
QY 225	IIRGLYKWTLMKTTTLVLAVASGLSGKEGPLVHVACCCGNIFSYLPKYSTNEAKKR	284		
Db 181	IIRGLYKWTLVIKITTLVLAVSSGLSGKEGPLVHVACCCGNITLCHCKRKNNEAKR	240		
QY 285	EVLASAASGAVSVAAGAPIGVLFSELYSYEFPKLTMRSPFALVAFVLRSTNPFEN	344		
Db 241	EVLASAASGAVSVAAGAPIGVLFSELYSYEFPKLTMRSPFALVAFVLRSTNPFEN	300		
QY 345	SRLYEVEYETPWTYLFELFEPILIGVEGGLMGAFFIRANIAMCRKRSTKGGKYPVLEV	404		
Db 301	SRLYEVEYETPWTYLFELFEPILIGVEGGLMGAFFIRANIAMCRKRSTKGGKYPVLEV	360		
QY 405	IIVAAITAVIAFPNPYTPNLNSELIKELFTDCGPLLESSLCDYRNDMAKTIVDIPDR	464		
Db 361	LIVAITIILAFPNPEYTRMSTSELSEFNDCGLDSSKLCYENHFNFTSK -GGELPDR	419		
QY 465	AGIGVYSIMOLCLAIKTIITVYTPFGIKVPSGLFTSMALGATAGRIYVGLAVDELAY	524		
Db 420	AGVGVYSIMOLCLAIKTIITVYTPFGIKVPSGLFTSMALGATAGRIYVGLAVDELAY	479		
QY 525	HHHDFIEKEMCEVGADCTTGPLYAMVGAACIGYTRMTVSVLVIVFELTGLELEYIVPM	584		
Db 480	HHHDFIEKEMCEVGADCTTGPLYAMVGAACIGYTRMTVSVLVIVFELTGLELEYIVPM	539		
QY 585	AAVMTSKVVGAFGREGIYEAHIRLNGYRPELDAKEEPTHHTLADVMRPRRNDPLAVLT	644		
Db 540	AAVMTSKVVGAFGREGIYEAHIRLNGYRPELDAKEEPTHHTLADVMRPRRNDPLAVLT	599		
QY 645	ODNMTVDDIEEMINTEVNGCFPVIMSKRSORVGFALRRDLTALIESARKKQEGIVGSR	704		
Db 600	ODNMTVDDIEEMINTEVNGCFPVIMSKRSORVGFALRRDLTALIESARKKQEGIVGSR	659		
QY 705	VCEAHPTEVLEPAESBRLKRSILDMSEPTVTDHTPMEIYVDIFRKLGRQCLVTHNGRL	764		
Db 660	IYFHEHSPMPRPYTPPLTKRLNIIDLSPFTVTDTPMEIYVDIFRKLGRQCLVTHNGRL	719		
QY 765	LGITTKDILHHMGTANODPASIMEN 791			
Db 720	LGITTKDVLKHIADMANODESILEN 746			

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RESULT 10
ID CLC5_MOUSE STANDARD: PRT: 746 AA.
AC Q9WVDA: 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 5 (CLC-5).
GN CLC5 OR CLC5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99303559; PubMed=10373326;
RA Tanaka K., Fisher S.E., Craig I.W.;
RT "Characterization of novel promoter and enhancer elements of the mouse
RT homologue of the Dent disease gene, CLCN5, implicated in X-linked
RT hereditary nephrolithiasis."
RT Genomics 58:281-292(1999).
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN RENAL
CC TUBULAR FUNCTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: KIDNEY-SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC
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CC
CC EMBL: AF134117; AAD8473.1;
CC MGD: MGI:99486; Clcn5.
CC InterPro: IPR001807; Cl-channel_volt.
CC DR Pfam: PF00571; CBS_2.
CC DR Pfam: PF00654; voltage_CLC_1.
CC DR PRINTS: PR00762; CLCHANNEL.
CC SMART: SM00116; CBS_2.
CC
CC Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
CC CBS domain; Repeat.
KW FT TRANSMEM 55 POTENTIAL.
KW FT TRANSMEM 133 153 POTENTIAL.
KW FT TRANSMEM 189 209 POTENTIAL.
KW FT TRANSMEM 246 266 POTENTIAL.
KW FT TRANSMEM 317 337 POTENTIAL.
KW FT TRANSMEM 352 372 POTENTIAL.
KW FT TRANSMEM 428 448 POTENTIAL.
KW FT TRANSMEM 453 473 POTENTIAL.
KW FT TRANSMEM 494 514 POTENTIAL.
KW FT TRANSMEM 521 541 POTENTIAL.
KW FT DOMAIN 585 614 CBS 1.
KW FT DOMAIN 682 733 CBS 2.
KW SEQUENCE 746 AA; 83100 MW; D8F3AE4FC331A08 CRC64;

Query Match 75.1%; Score 3137.5; DB 1; Length 746;
Best Local Similarity 76.6%; Pred. No. 7.5e-217;
Matches 572; Conservative 85; Mismatches 89; Indels 1; Gaps 1;

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DB 61 MLILGLSLAGLIDLSAHMTDLKREGICTGCFMFNEHCMSSEHVFHRDCKPEMN 120
QY 165 TWAEILIGQAEFGPSYIMNYIMYIFWALSFPAVLSKYVAPACSGIPEITILSGF 224
DB 121 SWAOLINFTDGAFAVYIVNPMYVLMALLFAFLAVLSLKAPACSGIPEITILSGF 180
QY 225 IIRGLGKWTMIKITYTLVLAVASGLSGKGPVHVACCNGINFSYLPFKYSTNEAKR 284
DB 181 IIRGLGKWTIVITITVLAVASGLSLGKGPVHVACCNGINILCHCFNKRNEAKR 240
QY 285 EVLSAASAGVAVFAGDIGVLFSEEVSYFPLKTLMSRFPAALVAFLVRSINPFGN 344
DB 241 EVLSAASAGVAVFAGDIGVLFSEEVSYFPLKTLMSRFPAALVAFLVRSINPFGN 300
QY 345 SRLVLFVEYHTPTVLPFLPFILLVGVGGIMGAFPTIRANIMCRKSTFGYVPLEV 404
DB 301 SRLVLFVEYHTPTVLPFLPFILLVGVGGIMGAFPTIRANIMCRKSTFGYVPLEV 360
QY 405 IIVAFIVAFVFPNRYRLNLTSELKELFTDCGPLSESSLCDYRNDMNAKRIVDIDPR 464
DB 361 LIVAFIVAFVFPNRYRLNLTSELKELFTDCGPLSESSLCDYRNDMNAKRIVDIDPR 419
QY 465 AGIGVSAIMQLALFKIIMTVFTGIRKVPQGLFTPSMAIGAIAGRIVGIAYEOLAVY 524
DB 420 AGVIGYSAMQALTLILKIVITITFTFGMKIPSGLFTPSMAVGAIGRLVGMEOQLAY 479
QY 525 HHMFIFKMEQVADCTPGLYAMVGAACLGVTMTVSLVYIVELTGLLEYIPLM 584
DB 480 HHMFIFKMEQVADCTPGLYAMVGAACLGVTMTVSLVYIVELTGLLEYIPLM 539
QY 585 AAVMTSKWGDPAFREGIEYEAHILNGYFPLDAKEEFTHTLADVVRPRNDPLAVLT 644
DB 540 AAVMTSKWVADALREGIYDHIILNGYFPLDAKEEFTHTLADVVRPRNDPLAVLT 599
QY 645 QDNATVDDIENIMETSYNGFPVYMSKESQRLVGFALRDLTIAIESARKKQESIVGSR 704
DB 600 QDNATVDDIENIMETSYNGFPVYMSKESQRLVGFALRDLTIAIESARKKQESIVGSR 659
QY 705 VCFQHPPLSPAPSPRLKLSIDMSFVTHDTPMEIYVDIRKGLRQCLVTHNGRL 764
DB 660 IYFTEHSPMPPTPLKLNITIDLSFVYTDLTPEIYVDIRKGLRQCLVTHNGRL 719
QY 765 LGIITKKDILRHMAQTANODPASIMFN 791
DB 720 LGIITKKDILRHMAQTANODPASIMFN 746

RESULT 11
ID GEF1_YEAST STANDARD: PRT: 779 AA.
AC P37020;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE GEF1 protein (Voltage-gated chloride channel) (CLC-Y1) (CLC-A).
GN GEF1 OR CLCY1 OR YJ0404W OR J1616.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94088447; PubMed=7505388;
RA Greene J.R., Brown N.H., Didomenico B.J., Kaplan J., Elde D.J.;
RT "The GEF1 gene of Saccharomyces cerevisiae encodes an integral
RT membrane protein; mutations in which have effects on respiration and
RT iron-limited growth."
RT Mol. Gen. Genet. 241:542-553(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;

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RX MEDLINE=95018225; PubMed=7932715;
RA Huang M.-E., Chuat J.-C., Galibert F.;
RT "A voltage-gated chloride channel in the yeast Saccharomyces
RT cerevisiae.";
RL J. Mol. Biol. 242:595-598(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RX MEDLINE=95397595; PubMed=7668047;
RA Huang M.-E., Chuat J.-C., Galibert F.;
RT "Analysis of a 42.5 kb DNA sequence of chromosome X reveals three
RT tRNA genes and a 12 new open reading frames including a gene most
RT probably belonging to the family of ubiquitin-protein ligases.";
RL least 11:775-781(1995).
CC -1- FUNCTION: TRANSPORT PROTEIN INVOLVED IN INTRACELLULAR IRON
CC METABOLISM DURING GROWTH ON FERMENTABLE AND NON FERMENTABLE CARBON
CC SOURCES. POTENTIAL VOLTAGE-GATED CHLORIDE CHANNEL.
CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: TO E.COLI YAD0 AND TO CHLORIDE CHANNEL PROTEINS.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
CC DR EMBL: 223117; CAA80663.1; -
CC DR EMBL: L29347; AAA53389.1; -
CC DR EMBL: 249540; CAA89387.1; -
CC DR EMBL: L36344; AAA8741.1; -
CC DR PIR: S39904; S39904.
CC DR SGD: S0003801; GEF1.
CC DR InterPro: IPR000644; CBS domain.
CC DR InterPro: IPR001807; Cl-channel_volt.
CC DR Pfam: PF00571; CBS; 2.
CC DR Pfam: PF00654; Voltage_CLC; 1.
CC DR PRINTS: PR00762; CLCHANNEL.
CC DR SMART: SM00116; CBS; 2.
CC KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
CC KW CBS domain; Repeat.
CC FT TRANSMEM 76 POTENTIAL.
CC FT TRANSMEM 155 175 POTENTIAL.
CC FT TRANSMEM 178 198 POTENTIAL.
CC FT TRANSMEM 204 224 POTENTIAL.
CC FT TRANSMEM 265 285 POTENTIAL.
CC FT TRANSMEM 337 357 POTENTIAL.
CC FT TRANSMEM 437 457 POTENTIAL.
CC FT TRANSMEM 489 509 POTENTIAL.
CC FT TRANSMEM 521 541 POTENTIAL.
CC FT DOMAIN 589 652 CBS 1.
CC FT DOMAIN 686 738 CBS 2.
CC FT CONFLICT 13 R->G (IN REF. 2).
CC FT CONFLICT 207 207 L->F (IN REF. 2).
CC FT CONFLICT 257 257 T->S (IN REF. 2).
CC FT CONFLICT 262 262 L->I (IN REF. 2).
CC FT CONFLICT 497 497 I->T (IN REF. 2).
CC SQ SEQUENCE 779 AA; 87682 MW; 56D86B3DE2FE25C CRC64;

Query Match 23.9%; Score 996.5; DB 1; Length 779;
Best Local Similarity 32.8%; Pred. No. 1,1e-63;
Matches 254; Conservative 151; Mismatches 253; Indels 117; Gaps 25;

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QY 155 EERDKCPQ---WKTAEELITGAEGPGSYIMNYIMIALSFAFLAVSLVAFYACG 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 137 ROFECEAGLWIAWK-----GHVSPEIIFMLSVLFALISTLVKXVAMAG 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 212 SGIPKEITLISGF-IIRGLKWTLMKITITVLAASGLSGKEBPLHVACCNNIFS 270
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 186 SGISEIKVWSGFEYNKEFELGLTLVIKSVLPLAISSGLSVGKEBSPVYATCC- 241
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 271 YLFPK-----YSTNEAKKREVLSAASAGSVAFGAPIGCVLESTEEV--SYFPLK 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 242 YLTKMLRLDTLYSR-----QYELTAAGACVAAFGAPIGCVLESTEEV--SYFPLK 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 321 TLWRSFALVAEYVLRSLNPGNSRLVFEYEHYTPWYLFELPEPILLVGFGMGAF 380
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 298 TLWRSYVALVATLTKYIDPFRNGRVLIFNVTYDRDMQVEIPIFALGIFGLGKYI 357
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 381 IRANIAMCRKRSKRGKPVLEIVIAATVIAFPNRYTRINSELKELTDCGPLE 440
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 358 SKWNINFIHFRK-WYSSMPVOEVLAVLTALISTFNEFLKIDMESGLIFHECVKND 416
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 441 SSS-----LCDYRNDMNAKIVDDIPDPAGIGVSAIMQLALIFKIMVTFGIRV 495
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 417 NNTSPSHRLCGDENTHAEPL-----KIFTSICEATYIRALLVVSYGARV 463
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 496 PGLFLPSAIGALAGRIAGVLAAYHDMFTFKWCEVAGADCTPGLYAMGAAC 555
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 464 PAGIFVPSAVGATGFAVSLVER-----FI-----SGPSVIIGAVAFGLGAAT 509
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 556 LGGVTRMYSIVVLELFGLEIVPLMAAVTSKWGDAG-RCGIYEAHRLMGYCF 614
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 510 LSGITNLTLVVVIMELGAFMYIIPLMIVVATIRILISTSGISGIDOMIMVGPY 569
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 615 L-----DAKEEFTHTLAADVMPRRNDPLAVLTODNMTVDIENMI---NETSYNCP 666
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 570 LDEQDEEEEFLEKXTAQIMSK-----LITINTIYLSLESLIYXSASYSVHGCP 624
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 667 VIMSK-----SRLVGFALRLDT--IAIESARKQEGIVGSSRCEAOTPSLPASER 720
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 625 ITRKDEKFEKERKICGYVLKRLHASKIMQSVNSTR--AQTLVYFNKSNEL-CHREN 680
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 721 PLKRSILDMSPFTYDTHPMELVDFRKLGLRGLVHNHNRGLGITRKQILR 775
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 681 GIGFQDMNESPIYKAVPVLFRFRELCKTIIVEESGLGLVYAKDILR 735
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
CLC7_MOUSE STANDARD; PRT: 803 AA.
ID CLC7_MOUSE
AC 070496;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 7 (CLC-7).
GN CLCN7 OR CLC7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21124827; PubMed=11207362;
RA Kornak U., Kasper D., Bosl M.R., Kaiser E., Schweizer M., Schulz A.,
RA Friedrich W., Delling G., Jentsch T.J.;
RT "Loss of the CLC-7 chloride channel leads to osteopetrosis in mice
RT and man.";
RL Cell 104:205-215(2001).
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.

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Db      458 NSMAAFENPEKSVLSLHDP-----GSYNMTIGLEFLVY-FFLAQWTYGLTVSAGVFI 513
Oy      502 PSMAIGALAGIVGIAVEOLAYTHHDWFIEKEWCEVGADCTPGLTYAMVGAACLGVTYR 561
Db      514 PSLIIGAMGRLFGFISLSYLT-----GAAIMVD---PKRYALMGAAADGGITVR 559
Oy      562 MYSVLVVVFELTGLGLEIVPLMAAVMTSKMVGAFEGEYIEAHIRNGVPFLDAKEEF 621
Db      560 MTLSITYIMMATISNVNTYGPIMLVLMTRAKLYGVDF-IEGLDMDHIQDSVPFLHWAPV 618
Oy      622 T-HTTLADVRRPRNRNDPLAVALTDQNMKYVDIEDINMET--SYNGEPVIY----SKESQR 675
Db      619 TSHSLTAREVW-----STPYTCILRR-BEKVGIIVDVLDSDTSNHNHGFPYEDVDGTOPAR 672
Oy      676 LVGVALRDLLIALIESARKKOEGIVSGSRVCFAQHT-----PSLPK----- 716
Db      673 LOGLIHSQLVLL-----KHKFEVERSNMGLVORRLKLKDFRAYIPFRPIQSIIWSQD 727
Oy      717 ESPPLKLRSLIDMSPTVDTHTPMETVIDYDFERRKIGLROCLVTNH-GRLLGIYTKDLIR 775
Db      728 ERECTMDLSEFMNSPVTYPQEASLPBYFKLFALGLRHLYVNDDNNHQVGLVTRYKDLAR 787
Oy      776 H-----MAQT 780
Db      788 YRLKGGLLELSLAOT 803

RESULT 13
CIC7_RAT STANDARD; PRT: 803 AA.
ID CIC7_RAT ID
AC P51799;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 7 (Clc-7).
GN CLCN7
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96130311; PubMed=8543009;
RA Brandt S., Jentsch T.D.;
RT "Clc-6 and Clc-7 are two novel broadly expressed members of the Clc
RT chloride channel family.";
RL FEBS Lett. 377:15-20(1995).
CC -! FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHelial TRANSPORT.
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! TISSUE SPECIFICITY: BRAIN, TESTIS, MUSCLE AND KIDNEY.
CC -! SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -! SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL; Z67744; CAA91557.1; -.
DR Interpro; IPR000644; CBS_domain.
DR Interpro; IPR001807; Cl-channel_volt.
DR Pfam; PF00571; CBS; 2
DR Pfam; PF00654; voltage_Clc; 1
DR PRINTS; PR00762; CLCHANNEL.
DR SMART; SM00116; CBS; 2.

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DR MIT; 602727; -.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl-channel_volt.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; Voltage_CIC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW CBS domain; Repeat.
FT TRANSMEM 128 148 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT TRANSMEM 224 244 POTENTIAL.
FT TRANSMEM 292 312 POTENTIAL.
FT TRANSMEM 375 395 POTENTIAL.
FT TRANSMEM 412 432 POTENTIAL.
FT TRANSMEM 495 515 POTENTIAL.
FT TRANSMEM 518 538 POTENTIAL.
FT TRANSMEM 581 601 POTENTIAL.
FT DOMAIN 629 674 CBS 1.
FT DOMAIN 739 783 CBS 2.
FT CONFLICT 267 267 T -> S (IN REF. 3).
FT CONFLICT 279 279 F -> L (IN REF. 3 AND 4).
SQ SEQUENCE 805 AA; 88679 MW; E56BC0BADAELC695 CRC64;

Query Match 17.98; Score 748.5; DB 1; Length 805;
Best Local Similarity 29.88; Pred. No. 6.3e-46;
Matches 237; Conservative 131; Mismatches 241; Indels 185; Caps 36;

OY 75 ERHRINSKKESAMENTKSLYDAMSGMLVLTGLASGALGLDIAADMTLKSGIC 134
| ||| : : : : : : : : : : : : : : : : : : : : : : : :
DB 109 EEEERIN---HTAFRVER-----KRWICALGLGLVACTDIYVELAGLKRVT 159
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 135 LSLALYNHEDOCWMSNTEFEERDKCPQMKWAEIIGQAEPSYIMNYIMYIFMA-LS 193
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 160 -----KGNDKFEK-----GGLSFSL-----LLMFTLN 183
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 194 FAPLAVS--LVKVPAPACSGDPEITILSGFIIRGLGKWTMTITLVLAVASGLS 251
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 AAFVLVSVAFLPEVPAAGSGIPQICFNGVKIPHVRLKTLVIVSGVILSVVGLA 243
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 252 LGRGPIVHVAOCGNGIES-----YLPKYSNEAKKREVLASAAGSV 297
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 244 VGRKGPPIH-----SGYIAGISGRSTSLKRFKIFEFRRDEKDFVSAGAAAGSA 299
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 298 AFGAPIGVLFSLSEVSYEPPLKTLMSFFALVAALVLSINPF--GN-----SRLVL 349
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 300 AFGAPVGVLFSLSEAGSFMNQFLTWRFASMTFTLNVLSITYGNMMDLSSPGLIN 359
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 350 F--YVEHTHWYLFELFPFILLGVFGIGMGAFPRANIAMCRKRSKTFG-KY-----P 400
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 360 FGREDSEKMAVTHIEIPVFTAMGVGVGLVAFNALNY-WL-----TMFRLRYIHRPCLQ 413
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 401 VLEVIYAATVAIVAFNPPTRLNTSELIKELFTDCGPLESSSL-----C--DYRND 450
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 414 VIEAVLAAVTAIVAFVLIYS-----RDCOPLOGGSSTYPLQFCADGET-NS 461
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 451 MNAS-----KIYDDIPDRPAGIGVYSATWOLCLALIFKLIMTVFTFGIKVPSGLETPS 503
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 462 MAFAFNTPEKSVSLFCHDP--GSYNPLTLGLFTLVY--FELACWTVYGLTVSAGVFLPS 517
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 504 MARGAIGRIVGLAVEDOLAYHHDMFLFKEMCEVAGDCITPGLYAMGAACLAGVTRMT 563
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 518 LLGGAAGRGLFGLISLYLT-----GAATWAD--PGKYALMGAAAOLOGIVRMT 563
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 564 VSLVIVFELTGLGLEYIVPLAAVMTSKWYGDAFGREGIYEAHIRLNGYPLAKKEFT- 622
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 564 LSLFLVIMTEATSNVTFPPLMLVLMYAKIVGVDF-IGSLDMHQLQSVPLHMEAVTS 622
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 623 HTTLADVMPRRNDPLAVLTODNMVVDIENMINET--SYNGFPYIM--SKESORLV 677
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 623 HSLTAREVM---STPYTCLRRKRGV--IVDVLSTASHNNGFPVVEHADTPQPARLQ 676
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 678 GFALRDLTLTAIESARKKQEGIVSSRVCRAQHT-----PSLPA-----ES 718
| : : : : : : : : : : : : : : : : : : : : : : : :

```

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DB 677 GLILRSQILVL-----KHKVVERSNGLVQRRLRKDFRDAYRPPPIIOSIHVSODER 731
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 719 PRPLKLSILDMSPFTYDTHPMETIYVDIFPKLGLRQCLVTHN--GRLLGITTKKDIIRH- 776
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 732 ECTMDLSEFMNPSPTVYPOEASLPRVFKRLFRALRLHLYVDNKNVYGLTRDLARIR 791
| : : : : : : : : : : : : : : : : : : : : : : : :
OY 777 -----MAQT 780
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 792 LGRKGLLELSLAQT 805
| : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
CLC6_HUMAN STANDARD; PRT; 869 AA.
AC P51797; P78521; O60818; O60819; O60820; O60821; Q99427; Q99428;
AC Q99429; P78520;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 6 (CLC-6).
GN CLCN6 OR KIAA0046.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RX MEDLINE=96130311; PubMed=8543009;
RA Brandt S., Jentsch T.J.;
RT "CLC-6 and CLC-7 are two novel broadly expressed members of the CLC
RT chloride channel family.";
RL FEBS Lett. 377:15-20(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D), AND SEQUENCE OF 1-409 FROM
RP N.A. (ISOFORM A).
RC TISSUE=Chronic myeloid leukemia cell;
RX MEDLINE=97344267; PubMed=9224655;
RA Egermont J., Buysse G., Voets T., Tylgat J., De Smedt H.,
RA Broeckmans G., Milius B.;
RT "Alternative splicing of CLC-6 (a member of the CLC chloride-channel
RT family) transcripts generates three truncated isoforms one of which,
RT CLC-6c, is kidney-specific.";
RL Biochem. J. 325:269-276(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX PubMed=10500249;
RA Kornak U., Boesi M.R., Kubisch C.;
RT "Complete genomic structure of the CLCN6 and CLCN7 putative chloride
RT channel genes.";
RL Biochim. Biophys. Acta 1447:100-106(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RA Ohara O., Nagase T., Kikuno R., Nomura N.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 50-869 FROM N.A., AND ALTERNATIVE SPLICING.
RA Errington H.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 237-869 FROM N.A. (ISOFORM A).
RC TISSUE=Bone marrow;
RX MEDLINE=96051398; PubMed=7584044;
RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
RA Seki N., Kawarabayashi Y., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. II.
RT The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by
RT DNA Res. 1:223-229(1994).
RN [7]
RP TISSUE SPECIFICITY.

```

RC TISSUE-Vascular smooth muscle, and Aortic endothelium;  
 RX MEDLINE=99222497; PubMed=10198195;  
 RA Lamb F.S., Clayton G.H., Liu B.-X., Smith R.L., Barna T.J.,  
 RA Schulte B.C.;  
 RT "Expression of CLCN voltage-gated chloride channel genes in human  
 RT blood vessels.";  
 RL J. Mol. Cell. Cardiol. 31:657-666(1999).  
 CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE  
 CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;  
 CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND  
 CC TRANSEPITHELIAL TRANSPORT.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; A/Clic-6a (shown here), B/Clic-  
 CC 6b/D2-A1, C/Clic-6c/D1-A1 and D/Clic-6d/D1-A2; are produced by  
 CC alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Testis, ovary, small intestine, brain and  
 CC skeletal muscle. Low level expression in aortic and coronary  
 CC vascular smooth muscle cells, and aortic endothelial cells.  
 CC Isoform C is only detected in kidney.  
 CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL: X83378; CAA58292.1; -  
 DR EMBL: X96391; CAA65255.1; -  
 DR EMBL: X99472; CAA67835.1; -  
 DR EMBL: X99473; CAA67836.1; -  
 DR EMBL: X99474; CAA67837.1; -  
 DR EMBL: X99475; CAA67838.1; -  
 DR EMBL: AF009257; AAB69287.1; -  
 DR EMBL: AF009247; AAB69287.1; JOINED.  
 DR EMBL: AF009248; AAB69287.1; JOINED.  
 DR EMBL: AF009249; AAB69287.1; JOINED.  
 DR EMBL: AF009250; AAB69287.1; JOINED.  
 DR EMBL: AF009251; AAB69287.1; JOINED.  
 DR EMBL: AF009252; AAB69287.1; JOINED.  
 DR EMBL: AF009253; AAB69287.1; JOINED.  
 DR EMBL: AF009254; AAB69287.1; JOINED.  
 DR EMBL: AF009255; AAB69287.1; JOINED.  
 DR EMBL: AF009256; AAB69287.1; JOINED.  
 DR EMBL: AL021155; CAA15951.1; -  
 DR EMBL: AL021155; CAA15952.1; -  
 DR EMBL: AL021155; CAA15953.1; -  
 DR EMBL: AL021155; CAA15954.1; -  
 DR EMBL: D28475; BAA05836.3; -  
 DR Gene: HGNC:2024; CLCN6.  
 DR MIM: 602726; -  
 DR InterPro: IPR000644; CBS\_domain.  
 DR InterPro: IPR001807; CL\_channel\_volt.  
 DR Pfam: PF00571; CBS; 2.  
 DR Pfam: PF00654; voltage\_CLC; 1.  
 DR PRINTS: PR00762; CLCHANNEL.  
 DR SMART: SM00116; CBS; 2.  
 KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;  
 KW CBS domain; Repeat; Alternative splicing.  
 FT TRANSMEM 82 102 POTENTIAL.  
 FT TRANSMEM 130 150 POTENTIAL.  
 FT TRANSMEM 164 204 POTENTIAL.  
 FT TRANSMEM 245 265 POTENTIAL.  
 FT TRANSMEM 334 354 POTENTIAL.  
 FT TRANSMEM 375 395 POTENTIAL.  
 FT TRANSMEM 462 482 POTENTIAL.  
 FT TRANSMEM 511 531 POTENTIAL.  
 FT DOMAIN 603 658 CBS 1.  
 FT DOMAIN 805 856 CBS 2.  
 FT DOMAIN 4 18 CYS-RICH.

FT VARSP LIC 237 320 DKRDVYSAAGAAAFAPAGTGLTFLSEEGSSFNNOGTL  
 FT FT KWVLFCSMSATFTLNFRSGTIOGSGMSFQPLNFEGERK  
 FT FT CS -> YGKROERLCTISRGSCWSCSGFRGARNRGYILOSRCG  
 FT FT FYLLERPAHVESALLFHVCHLHPQLLPFMDSVKCLFLPAP  
 FT FT WIALMRV (IN ISOFORM B).  
 FT FT CSDDSKRCHMTLGFVFMGVPVIGLIGATPNC -> SL  
 FT FT REPCVSGNRHRCVCCLDGVRMPDVLFEESNR (IN  
 FT FT ISOFORM C).  
 FT VARSP LIC 354 869 MISSING (IN ISOFORM C).  
 FT VARSP LIC 237 308 DKRDVYSAAGAAAFAPAGTGLTFLSEEGSSFNNOGTL  
 FT FT KWVLFCSMSATFTLNFRSGTIOGSGMSFQPLNFEGERK  
 FT FT CS -> YGKROERLCTISRGSCWSCSGFRGARNRGYILOSRCG  
 FT FT FYLLERPAHVESALLFHVCHLHPQLLPFMDSVKCLFLPAP  
 FT FT WIALMRV (IN ISOFORM B).  
 FT FT CSDDSKRCHMTLGFVFMGVPVIGLIGATPNC -> SL  
 FT FT REPCVSGNRHRCVCCLDGVRMPDVLFEESNR (IN  
 FT FT ISOFORM C).  
 FT VARSP LIC 309 869 MISSING (IN ISOFORM D).  
 FT CONFLICT 198 198 G -> E (IN REF. 5).  
 FT SEQUENCE 869 AA: 97216 MM: E423777D9FF4328 CRC64;  
 Query Match 17.4%; Score 725.5; DB 1; Length 869;  
 Best local Similarity 25.3%; Pred. No. 3,1e-44;  
 Matches 235; Conservative 142; Mismatches 245; Indels 307; Gaps 35;  
 QY 49 DEPIPGVGYDDHTIDWREKC-----KDERHRRIRNSKKESAMEKNTSLYD 97  
 DB 40 DEILP-----RKDESDLY--DRCINDPYLEVLETMDKKGRREAVK-----80  
 QY 98 AMGWLVVTLTLGASGALGLDIDADMWTDLKEGICLSLAWNHECCGMSNETFEER 157  
 DB 81 -----MMVFAIGCTGVLGVLPFVRLEFOLKFGVV-----QTSVE- 119  
 QY 158 DKCPQMKTWALLIGQAEGPSYIMNYITFALSAFLAVSLVWFAPYAGSGSIPET 217  
 DB 120 --CSQ-----KGLCALSLLELLGNLTFFVFLA-SLVLVLEBVAAGSGIPEV 162  
 QY 218 KTLISGFIINGYIGKWTLMKTTTLVLAASGLSGKEGPLVHVACCG-----266  
 DB 163 KCYLNGKVPYIVRLTLCKVGLFVSAGGLFVCEKPMHSGSVYAGLPQFOSISL 222  
 QY 267 NIFSYLEPFRKSTNEAKKREVLASAAGVAVFAGPILGVLFSLSESYVEPLKTLWRSF 326  
 DB 223 RKIQFNFP-YFRSDRDKRDVSAGAAVAAAFAPAGTGLTFLSEEGSSFNNOGTLKVL 261  
 QY 327 FAALVAFAVLR-----SINFGNSRL--VLFYVEVHTP-----WYLFELFPITLG 370  
 DB 282 FCSMSATFTLNFRSGTIOGSGMSFQPLNFEGERKCHMTMDLGFVYMG 341  
 QY 371 VEGGLMGAFPIRANIAMCRKRKSTK-----GKYP-----VLEVIYAATVIAFPNPT 421  
 DB 342 VIGLLGATFN-----CLNKRRLAKYRMVHPRKLVRLVLESILVSLVTVVVF-----390  
 QY 422 RLMTSELIKELFTDCGPLESSSLCDVRNMDNASKIYDDI-----460  
 DB 391 -----VASNVLECCROMSSS--QIGNDSFQLOVEDVAVSSIKTFPCPDYTDNMAITL 442  
 QY 461 --PDRPAGI-----GYVSAIMOLCLALFKILMTVEFTGIKVPSGLFTPSMAIGATGR 512  
 DB 443 FNPQESALTLQFLHQDGFSPV-TLALFEVLVELLACTYISVPSGLFVSLGCAAFGR 501  
 QY 513 IVCIAVEQLAYHHDMFIREKCEVGAADCTPGLYANVGAACLGVTNRVSLVAVFE 572  
 DB 502 LVANVLKSY-----IGIGHYVSGTFAALGAALGVGVRMTISLTVLLIE 546  
 QY 573 LRGLEIYVLMVAVMTSKVGDAFEGEYEAHIRNGVPEFLDAKEEFHTTL--ADVM 631  
 DB 547 STNELITYGLPIVTLMAKWTGDFPNK-GTYDTHVGRGLVLEMETEVBMDKLRASDIM 605  
 QY 632 RPRRNDPLAVLTQDNMT-----VDLIEENMINETSYNGFVI-----668  
 DB 606 EP-----NLTYVYPHTRIQSLVSLRTYVHAAPVVTENRGNEKEPFMGNO 652  
 QY 669 -----MSKESQRLVGF--ALRR--DLTATIESARKQD-----697  
 DB 653 ISNNIKFKKSSILTRAGEORRKSQSMKSYPSSELRNMCDEHIASEPAEKEDLLOOMLER 712

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QY 698 -----GIVGSSR-----YCEAQHTPSPAPESP 719
Db 713 RYTPYPNLYPDQSPSEDWTEERFRPLTFHGLIRSQLVTLVARGCYSESQSS--ASQP 770
QY 720 R-----PLKLRSLIDM-----SPTVTDHTPMEIVVDIFRKL 751
Db 771 RLSTAEAAEDYPRYPDIHDLDTLLNPRMIVDTPPYMNPSPFTVSPNTHVSQVFNLFRTM 830
QY 752 GLROC-LVTNHRRLGILTCKDILRHMAQ 779
Db 831 GLRHLPPVMAVGEIVGIITRHNLTVEFLQ 859

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Search completed: May 12, 2003, 15:03:19  
 Job time : 31 secs